

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Seed, Brian et al.
- (ii) TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES AND METHODS
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Clark & Elbing LLP
  - (B) STREET: 585 Commercial Street
  - (C) CITY: Boston
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02109-1024
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/756,018
  - (B) FILING DATE: 25-NOV-96
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/661,960
  - (B) FILING DATE: 12-JUN-1996
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/000,213
  - (B) FILING DATE: 14-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Elbing, Karen Lech
  - (B) REGISTRATION NUMBER: 35,238
  - (C) REFERENCE/DOCKET NUMBER: 00786/284002
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 617/723-6777
  - (B) TELEFAX: 617/723-8962
  - (C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid

- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Thr Glu Ala Gln Thr Thr Pro Pro Ala  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Thr Asn Ser Leu Glu Thr Ser Thr Gly Thr Ser Gly Pro Pro  
1                      5                      10                      15

Val Thr

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu Gly Pro  
1                      5                      10                      15

Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp  
20                      25                      30

Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro  
35                      40

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg	Asp	Arg	Arg	Gln	Ala	Thr	Glu	Tyr	Glu	Tyr	Leu	Asp	Tyr	Asp	Phe
1				5					10					15	
Leu Pro Glu Thr															
20															

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg	Asp	Arg	Arg	Gln	Ala	Thr	Glu	Phe	Glu	Phe	Leu	Asp	Phe	Asp	Phe
1				5					10					15	
Leu Pro Glu Thr															
20															

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg	Asp	Arg	Arg	Gln	Ala	Ala	Glu	Tyr	Glu	Tyr	Leu	Asp	Tyr	Asp	Phe
1				5					10					15	
Leu Pro Glu Ala															
20															

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Arg	Asp	Arg	Arg	Gln	Ala	Ala	Glu	Phe	Glu	Phe	Leu	Asp	Phe	Asp	Phe
1				5					10					15	
Leu	Pro	Glu	Ala												
				20											

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2287 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGCTTACCA CCATGGACTG GACCTGGAGG TTCCTCTTCT TTGTGGTGGC AGCAGCTACA	60
GGTGTCCAGT CCCAGGTGCA GCTGGTGCAG TCTGGGGCTG AGGTGAAGAA GCCTGGGTCC	120
TCGGTGAAGG TCTCCTGCAA GGCTTCTGGA GGCACCTTCA GCAGCTATGC TATCAGCTGG	180
GTGCGACAGG CCCCTGGACA AGGGCTTGAG TGGATGGGAG GGATCATCCC TATCTTTGGT	240
ACAGCAAACCT ACGCACAGAA GTTCCAGGGC AGAGTCACGA TTACCGCGGA CGAATCCACG	300
AGCACAGCCT ACATGGAGCT GAGCAGCCTG AGATCTGAGG ACACGGCCGT GTATTACTGT	360
GCGAGAGATA ATGGAGCGTA TTGTAGTGGT GGTAGCTGCT ACTCGGGCTG GTTCGACCCC	420
TGGGGCCAGG GAACCCTGGT CACCGTCTCT TCAGGTGAGT ACTGAATTCT AGCTTTCTGG	480
GGCAGGCCAG GCCTGACCTT GGCTTTGGGG CAGGGAGGGG GCTAAGGTGA GGCAGGTGGC	540
GCCAGCAGGT GCACACCCAA TGCCCATGAG CCCAGACACT GGACGCTGAA CCTCGCGGAC	600
AGTTAAGAAC CCAGGGGCCT CTGCGCCTGG GCCCAGCTCT GTCCACACC GCGGTCACAT	660
GGCACCACCT CTCTTGACG CTCCACCAAG GGCCCATCGG TCTTCCCCCT GGCACCCTCC	720
TCCAAGAGCA CCTCTGGGGG CACAGCGGCC CTGGGCTGCC TGGTCAAGGA CTAATTCCCC	780

GAACCGGTGA CGGTGTCGTG GAACTCAGGC GCCCTGACCA GCGGCGTGCA CACCTTCCCG	840
GCTGTCCTAC AGTCCTCAGG ACTCTACTCC CTCAGCAGCG TGGTGACCGT GCCCTCCAGC	900
AGCTTGGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA CACCAAGGTG	960
GACAAGAAAG TTGGTGAGAG GCCAGCACAG GGAGGGAGGG TGTCTGCTGG AAGCAGGCTC	1020
AGCGCTCCTG CCTGGACGCA TCCCGGCTAT GCAGCCCCAG TCCAGGGCAG CAAGGCAGGC	1080
CCCGTCTGCC TCTTCACCCG GAGCCTCTGC CCGCCCCACT CATGCTCAGG GAGAGGGTCT	1140
TCTGGCTTTT TCCCAGGCTC TGGGCAGGCA CAGGCTAGGT GCCCCTAACC CAGGCCCTGC	1200
ACACAAAGGG GCAGGTGCTG GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC	1260
CCCTGACCTA AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT	1320
CTCCTCCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT CTTGTGACAA	1380
AACTCACACA TGCCACCGT GCCCAGGTAA GCCAGCCCAG GCCTCGCCCT CCAGCTCAAG	1440
GCGGGACAGG TGCCCTAGAG TAGCCTGCAT CCAGGGACAG GCCCCAGCCG GGTGCTGACA	1500
CGTCCACCTC CATCTCTTCC TCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCCTCT	1560
TCCCCCAAA ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACATGCGTGG	1620
TGGTGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG GACGGCGTGG	1680
AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA CAACAGCACG TACCGGGTGG	1740
TCAGCGTCCT CACCGTCCTG CACCAGGACT GGCTGAATGG CAAGGAGTAC AAGTGCAAGG	1800
TCTCCAACAA AGCCCTCCCA GCCCCATCG AGAAAACCAT CTCCAAAGCC AAAGGTGGGA	1860
CCCGTGGGGT GCGAGGGCCA CATGGACAGA GGCCGGCTCG GCCCACCCTC TGCCCTGAGA	1920
GTGACCGCTG TACCAACCTC TGTCTACAG GGCAGCCCCG AGAACCACAG GTGTACACCC	1980
TGCCCCATC CCGGGATGAG CTGACCAAGA ACCAGGTCAG CCTGACCTGC CTGGTCAAAG	2040
GCTTCTATCC CAGCGACATC GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAAC	2100
ACAAGACCAC GCCTCCCGTG CTGGACTCCG ACGGCTCCTT CTTCTCTAC AGCAAGCTCA	2160
CCGTGGACAA GAGCAGGTGG CAGCAGGGGA ACGTCTTCTC ATGCTCCGTG ATGCATGAGG	2220
CTCTGCACAA CCACTACAG CAGAAGAGCC TCTCCCTGTC TCCGGGTAAA TGAGTGCGAC	2280
GGCCGGC	2287

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys	Leu	Thr	Thr	Met	Asp	Trp	Thr	Trp	Arg	Phe	Leu	Phe	Phe	Val	Val
1				5					10					15	
Ala	Ala	Ala	Thr	Gly	Val	Gln	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly
			20					25					30		
Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala
			35				40					45			
Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr	Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala
	50					55					60				
Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly
65					70					75				80	
Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala
				85					90					95	
Asp	Glu	Ser	Thr	Ala	Arg	Asp	Asn	Gly	Ala	Tyr	Cys	Ser	Gly	Gly	Ser
			100					105					110		
Cys	Tyr	Ser	Gly	Trp	Phe	Asp	Pro	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr
		115					120					125			
Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro
		130				135					140				
Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val
145					150				155					160	
Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala
				165					170					175	
Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly
			180					185					190		
Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Asp	Lys
		195					200					205			
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
		210				215					220				

Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	225	230	235	240
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	245	250	255	
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	260	265	270	
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	275	280	285	
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	290	295	300	
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	305	310	315	320
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	325	330	335	
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	340	345	350	
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	355	360	365	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	370	375	380	
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	385	390	395	400
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	405	410	415	
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	420	425	430	
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys							435	440		

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGGCGCTGT CCTGGGTTCT TACAGTCCTG AGCCTCCTAC CTCTGCTGGA AGCCCAGATC	60
CCATTGTGTG CCAACCTAGT ACCGGTGCCC ATCACCAACG CCACCCTGGA CCAGATCACT	120
GGCAAGTGGT TTTATATCGC ATCGGCCTTT CGAAACGAGG AGTACAATAA GTCGGTTCAG	180
GAGATCCAAG CAACCTTCTT TTA CTTCACC CCCAACAAGA CAGAGGACAC GATCTTTCTC	240
AGAGAGTACC AGACCCGACA GGACCAGTGC ATCTATAACA CCACCTACCT GAATGTCCAG	300
CGGGAAAATG GGACCATCTC CAGATACGTG GGAGGCCAAG AGCATTTCGC TCACTTGCTG	360
ATCCTCAGGG ACACCAAGAC CTACATGCTT GCTTTTGACG TGAACGATGA GAAGAACTGG	420
GGGCTGTCTG TCTATGCTGA CAAGCCAGAG ACGACCAAGG AGCAACTGGG AGAGTTCTAC	480
GAAGCTCTCG ACTGCTTGCG CATTCCCAAG TCAGATGTCTG TGTACACCGA TTGGAAAAAG	540
GATAAGTGTG AGCCACTGGA GAAGCAGCAC GAGAAGGAGA GGAAACAGGA GGAGGGGGAA	600
TCGGATCCCG AGGGTGAGTA CTAAGCTTCA GCGCTCCTGC CTGGACGCAT CCCGGCTATG	660
CAGCCCCAGT CCAGGGCAGC AAGGCAGGCC CCGTCTGCCT CTTACCCCGG AGCCTCTGCC	720
CGCCCCACTC ATGCTCAGGG AGAGGGTCTT CTGGCTTTTTT CCCAGGCTCT GGGCAGGCAC	780
AGGCTAGGTG CCCCTAACCC AGGCCCTGCA CACAAAGGGG CAGGTGCTGG GCTCAGACCT	840
GCCAAGAGCC ATATCCGGGA GGACCCTGCC CCTGACCTAA GCCCACCCCA AAGGCCAAAC	900
TCTCCACTCC CTCAGCTCGG ACACCTTCTC TCCTCCCAGA TTCCAGTAAC TCCCAATCTT	960
CTCTCTGCAG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCACCGTG CCCAGGTAAG	1020
CCAGCCCAGG CCTCGCCCTC CAGCTCAAGG CGGGACAGGT GCCCTAGAGT AGCCTGCATC	1080
CAGGGACAGG CCCCAGCCGG GTGCTGACAC GTCCACCTCC ATCTCTTCCT CAGCACCTGA	1140
ACTCCTGGGG GGACCGTCAG TCTTCCTCTT CCCCCAAAA CCAAGGACA CCCTCATGAT	1200
CTCCCGGACC CCTGAGGTCA CATGCGTGGT GGTGGACGTG AGCCACGAAG ACCCTGAGGT	1260
CAAGTTCAAC TGGTACGTGG ACGGCGTGGA GGTGCATAAT GCCAAGACAA AGCCGCGGGA	1320
GGAGCAGTAC AACAGCACGT ACCGGGTGGT CAGCGTCCTC ACCGTCCTGC ACCAGGACTG	1380
GCTGAATGGC AAGGAGTACA AGTGCAAGGT CTCCAACAAA GCCCTCCCAG CCCCCATCGA	1440
GAAAACCATC TCCAAAGCCA AAGGTGGGAC CCGTGGGGTG CGAGGGCCAC ATGGACAGAG	1500
GCCGGCTCGG CCCACCCTCT GCCCTGAGAG TGACCGCTGT ACCAACCTCT GTCCTACAGG	1560
GCAGCCCCGA GAACCACAGG TGTACACCCT GCCCCATCC CGGGATGAGC TGACCAAGAA	1620



CCAGGTCAGC CTGACCTGCC TGGTCAAAGG CTTCTATCCC AGCGACATCG CCGTGGAGTG 1680  
 GGAGAGCAAT GGGCAGCCGG AGAACAACTA CAAGACCACG CCTCCCGTGC TGGACTCCGA 1740  
 CGGCTCCTTC TTCCTCTACA GCAAGCTCAC CGTGGACAAG AGCAGGTGGC AGCAGGGGAA 1800  
 CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC CACTACACGC AGAAGAGCCT 1860  
 CTCCTGTCT CCGGGTAAAT GAGTGCGACG GCCG 1894

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ala	Leu	Ser	Trp	Val	Leu	Thr	Val	Leu	Ser	Leu	Leu	Pro	Leu	Leu
1				5					10					15	
Glu	Ala	Gln	Ile	Pro	Leu	Cys	Ala	Asn	Leu	Val	Pro	Val	Pro	Ile	Thr
				20				25					30		
Asn	Ala	Thr	Leu	Asp	Gln	Ile	Thr	Gly	Lys	Trp	Phe	Tyr	Ile	Ala	Ser
				35				40				45			
Ala	Phe	Arg	Asn	Glu	Glu	Tyr	Asn	Lys	Ser	Val	Gln	Glu	Ile	Gln	Ala
				50			55				60				

Thr	Phe	Phe	Tyr	Phe	Thr	Pro	Asn	Lys	Thr	Glu	Asp	Thr	Ile	Phe	Leu	65	70	75	80
Arg	Glu	Tyr	Gln	Thr	Arg	Gln	Asp	Gln	Cys	Ile	Tyr	Asn	Thr	Thr	Tyr	85	90	95	
Leu	Asn	Val	Gln	Arg	Glu	Asn	Gly	Thr	Ile	Ser	Arg	Tyr	Val	Gly	Gly	100	105	110	
Gln	Glu	His	Phe	Ala	His	Leu	Leu	Ile	Leu	Arg	Asp	Thr	Lys	Thr	Tyr	115	120	125	
Met	Leu	Ala	Phe	Asp	Val	Asn	Asp	Glu	Lys	Asn	Trp	Gly	Leu	Ser	Val	130	135	140	
Tyr	Ala	Asp	Lys	Pro	Glu	Thr	Thr	Lys	Glu	Gln	Leu	Gly	Glu	Phe	Tyr	145	150	155	160
Glu	Ala	Leu	Asp	Cys	Leu	Arg	Ile	Pro	Lys	Ser	Asp	Val	Val	Tyr	Thr	165	170	175	
Asp	Trp	Lys	Lys	Asp	Lys	Cys	Glu	Pro	Leu	Glu	Lys	Gln	His	Glu	Lys	180	185	190	
Glu	Arg	Lys	Gln	Glu	Glu	Gly	Glu	Ser	Asp	Pro	Glu	Gly	Glu	Pro	Lys	195	200	205	
Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	210	215	220	
Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	225	230	235	240
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	245	250	255	
Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	260	265	270	
Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	275	280	285	
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	290	295	300	
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	305	310	315	320
Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	325	330	335	
Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	340	345	350	

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
 355 360 365  
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
 370 375 380  
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
 385 390 395 400  
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
 405 410 415  
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
 420 425 430  
 Leu Ser Pro Gly Lys  
 435

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 442 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Lys Leu Thr Thr Met Asp Trp Thr Trp Arg Phe Leu Phe Phe Val Val  
 1 5 10 15  
 Ala Ala Ala Thr Gly Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly  
 20 25 30  
 Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala  
 35 40 45  
 Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala  
 50 55 60  
 Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly  
 65 70 75 80  
 Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala  
 85 90 95  
 Asp Glu Ser Thr Ala Arg Asp Asn Gly Ala Tyr Cys Ser Gly Gly Ser  
 100 105 110

Cys Tyr Ser Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr  
 115 120 125  
 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
 130 135 140  
 Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
 145 150 155 160  
 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
 165 170 175  
 Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
 180 185 190  
 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Asp Lys  
 195 200 205  
 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
 210 215 220  
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
 225 230 235 240  
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
 245 250 255  
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Asn Phe Ser Trp  
 260 265 270  
 Tyr Val Asp Gly Val Glu Val His Asn Asn Lys Thr Lys Pro Arg Glu  
 275 280 285  
 Glu Asn Tyr Ser Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu  
 290 295 300  
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Asn Val Ser Asn  
 305 310 315 320  
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Asn Ile Ser Lys Ala Lys Gly  
 325 330 335  
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu  
 340 345 350  
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
 355 360 365  
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
 370 375 380

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
 385 390 395 400  
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
 405 410 415  
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
 420 425 430  
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 435 440

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro Glu Met Leu Arg Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly  
 1 5 10 15  
 Pro Gly Thr Pro Glu Ser Thr Thr Val Glu Pro Ala Ala Arg Arg Ser  
 20 25 30  
 Thr Gly Leu Asp Ala Gly Gly Ala Val Thr Glu  
 35 40

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu Ser Thr Asp Ser Ala  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids  
(B) TYPE: amino acids  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids  
(B) TYPE: amino acids  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Asp Tyr Glu Tyr Asp Glu Leu Pro  
1 5